

# Full wwPDB X-ray Structure Validation Report (i)

#### Jan 5, 2022 – 06:07 pm GMT

PDB ID	:	6ZHS
Title	:	Uba1 bound to two E2 (Ubc13) molecules
Authors	:	Misra, M.; Schindelin, H.
Deposited on	:	2020-06-23
Resolution	:	2.35  Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org* A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.24
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.24

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 2.35 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Motrie	Whole archive	Similar resolution
WIEUTIC	$(\# { m Entries})$	$(\# { m Entries},  { m resolution}  { m range}({ m \AA}))$
$R_{free}$	130704	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	$1211 \ (2.36-2.36)$
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain		
1	А	1024	8%	10%	•••
2	В	154	<b>6%</b> 84%	12%	••••
2	С	154	87%	11%	•



#### 6 Z H S

# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 21003 atoms, of which 10317 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called Ubiquitin-activating enzyme E1 1.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace	
1	А	994	Total 15631	C 5011	Н 7768	N 1299	O 1530	S 23	0	3	0

• Molecule 2 is a protein called Ubiquitin-conjugating enzyme E2 13.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
2	В	159	Total	С	Η	Ν	0	S	0	6	0
	D	152	2526	804	1272	214	233	3	0	0	0
0	C	151	Total	С	Η	Ν	Ο	$\mathbf{S}$	0	0	0
			2445	781	1229	204	228	3	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	0	GLY	-	expression tag	UNP P52490
С	0	GLY	-	expression tag	UNP P52490

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total         C         H         O           14         3         8         3	0	0
4	А	1	Total         C         H         O           14         3         8         3	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
4	Λ	1	Total	С	Η	0	0	0	
4 A	1	14	3	8	3	0	0		
4	Δ	1	Total	С	Η	0	0	0	
4	Л	1	14	3	8	3	0	0	
4	Λ	1	Total	С	Η	0	0	0	
4	4 A	1	14	3	8	3	0	0	
4 A	1	Total	С	Η	0	0	0		
	А	A I		3	8	3	0	0	

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	261	Total         O           261         261	0	0
5	В	21	Total O 21 21	0	0
5	С	25	Total O 25 25	0	0



## 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.



• Molecule 1: Ubiquitin-activating enzyme E1 1

• Molecule 2: Ubiquitin-conjugating enzyme E2 13

Chain C: 87% 11%





K151 PRO GLU



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	177.71Å 72.90Å 139.52Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $112.43^{\circ}$ $90.00^{\circ}$	Depositor
Bosolution (Å)	24.92 - 2.35	Depositor
	24.92 - 2.35	EDS
% Data completeness	66.2(24.92-2.35)	Depositor
(in resolution range)	66.2(24.92-2.35)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.37 (at 2.36 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
B B.	0.216 , $0.275$	Depositor
$\Lambda, \Lambda_{free}$	0.216 , $0.274$	DCC
$R_{free}$ test set	2266 reflections $(4.97%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	26.9	Xtriage
Anisotropy	0.641	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for $twinning^2$	$   <  L  > = 0.45, < L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	21003	wwPDB-VP
Average B, all atoms $(Å^2)$	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.32% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 5 Model quality (i)

## 5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mal	Chain	Bond lengths		Bond angles		
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.26	0/8033	0.44	0/10869	
2	В	0.26	0/1312	0.50	1/1784~(0.1%)	
2	С	0.25	0/1246	0.45	0/1696	
All	All	0.26	0/10591	0.45	1/14349~(0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	4	LEU	CA-CB-CG	6.55	130.36	115.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	7863	7768	7758	54	0
2	В	1254	1272	1242	14	0
2	С	1216	1229	1231	5	0
3	А	10	0	0	0	0
4	А	36	48	48	2	0
5	А	261	0	0	0	0
5	В	21	0	0	0	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	С	25	0	0	0	0
All	All	10686	10317	10279	68	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (68) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom_1	Atom_2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:493:ASN:HB3	1:A:517:ILE:HD11	1.68	0.74
1:A:71:VAL:HG22	1:A:91:ARG:HG2	1.74	0.69
2:B:4:LEU:HD13	2:B:5:PRO:HD3	1.76	0.67
1:A:444:ALA:HB1	1:A:870:THR:HG21	1.77	0.66
1:A:71:VAL:HG23	1:A:89:GLN:O	1.98	0.63
1:A:558:PHE:O	1:A:930:ARG:NH1	2.32	0.62
1:A:294:LEU:HB3	1:A:326:VAL:HG13	1.82	0.61
1:A:958:SER:HB3	2:B:9:ILE:HD11	1.82	0.61
1:A:413:VAL:HG12	1:A:413:VAL:O	2.01	0.59
1:A:702:SER:O	1:A:703:ASN:HB2	2.03	0.59
1:A:544[B]:ASP:O	1:A:545[B]:ASN:CB	2.51	0.59
1:A:963:LEU:HB2	2:B:32:LEU:HD11	1.86	0.58
1:A:958:SER:CB	2:B:9:ILE:HD11	2.33	0.58
1:A:517:ILE:O	1:A:517:ILE:HG23	2.04	0.58
1:A:450:LEU:HB3	1:A:502:VAL:HG11	1.88	0.55
1:A:568:THR:HG22	1:A:873:VAL:HG21	1.89	0.54
1:A:50:GLU:O	1:A:54:ASN:ND2	2.42	0.52
1:A:410:THR:O	1:A:410:THR:HG23	2.09	0.52
1:A:155:GLU:OE1	1:A:300:HIS:NE2	2.40	0.51
1:A:454:ALA:HA	1:A:509:LEU:HD11	1.91	0.51
1:A:958:SER:OG	2:B:9:ILE:HD11	2.12	0.49
1:A:27:GLY:HA3	4:A:1103:GOL:H12	1.94	0.49
1:A:437:VAL:HG11	1:A:453:TRP:CH2	2.47	0.49
1:A:311:PRO:O	1:A:356:ARG:NH1	2.46	0.49
1:A:169:ASP:O	1:A:265:SER:OG	2.21	0.48
1:A:1000:THR:HA	1:A:1022:ILE:O	2.14	0.48
2:B:4:LEU:N	2:B:5:PRO:CD	2.77	0.47
1:A:493:ASN:CB	1:A:517:ILE:HD11	2.40	0.47
2:B:58:LEU:HD11	2:B:101:ILE:HD11	1.97	0.47
1:A:320:ASN:HA	1:A:323:ILE:HD12	1.95	0.46
1:A:590:ARG:CZ	1:A:590:ARG:HB2	2.44	0.46
1:A:634:TYR:OH	1:A:806:PRO:O	2.33	0.46



Atom-1	Atom-2	Interatomic	Clash
Atom-1	At0111-2	distance (Å)	overlap (Å)
1:A:36:THR:O	1:A:36:THR:CG2	2.62	0.46
1:A:650:ASP:O	1:A:654:VAL:HG23	2.16	0.46
1:A:544[B]:ASP:O	1:A:545[B]:ASN:HB3	2.16	0.46
2:C:121:LEU:HD12	2:C:121:LEU:N	2.30	0.46
1:A:880:GLU:OE2	1:A:895:LYS:N	2.47	0.45
1:A:588:SER:HA	2:B:1:MET:HG2	1.99	0.45
1:A:50:GLU:HB3	1:A:367:GLY:HA3	1.99	0.45
2:C:124:ASP:O	2:C:127:GLU:HG2	2.18	0.44
1:A:917:GLY:O	1:A:923:LYS:HG3	2.17	0.44
1:A:1002:ILE:HG23	1:A:1019:PHE:CD2	2.53	0.44
1:A:285:LYS:NZ	1:A:395:GLU:OE1	2.46	0.44
1:A:309:GLU:OE2	1:A:356:ARG:NH2	2.50	0.43
2:B:4:LEU:HD13	2:B:5:PRO:CD	2.48	0.43
2:B:120:PRO:HB3	2:B:126:ALA:CB	2.47	0.43
1:A:410:THR:O	1:A:410:THR:CG2	2.66	0.43
1:A:628:ALA:HA	1:A:816:LEU:HD12	2.00	0.43
1:A:128:ALA:O	1:A:153:SER:HA	2.18	0.43
2:C:53:GLU:C	2:C:54:LEU:HD12	2.38	0.43
1:A:381:LYS:O	1:A:382:PHE:HB2	2.19	0.43
1:A:29:GLU:H	4:A:1103:GOL:H31	1.84	0.42
1:A:541:ASN:ND2	1:A:565:GLU:OE2	2.52	0.42
1:A:961:VAL:HG13	1:A:961:VAL:O	2.19	0.42
1:A:435:SER:HB2	1:A:458:LEU:CD1	2.49	0.42
1:A:517:ILE:O	1:A:517:ILE:CG2	2.67	0.42
1:A:22:GLN:OE1	1:A:58:ALA:HA	2.19	0.41
2:C:54:LEU:HD12	2:C:54:LEU:N	2.35	0.41
1:A:641:VAL:HG23	1:A:642:GLU:N	2.35	0.41
1:A:444:ALA:HB2	1:A:481:ARG:HG3	2.01	0.41
1:A:584:GLU:HA	1:A:927:ILE:HD13	2.03	0.41
1:A:160:PHE:CZ	1:A:394:LEU:HD21	2.56	0.41
2:B:120:PRO:HB3	2:B:126:ALA:HB2	2.03	0.41
2:B:41:GLY:HA3	2:B:47:TYR:O	2.21	0.40
2:C:8:ILE:HG21	2:C:32:LEU:HG	2.03	0.40
1:A:313:THR:HG22	1:A:410:THR:HG21	2.04	0.40
2:B:62:TYR:CD1	2:B:63:PRO:HA	2.56	0.40

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There are no symmetry-related clashes.



## 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perc	entiles
1	А	993/1024~(97%)	942 (95%)	46 (5%)	5 (0%)	29	32
2	В	156/154~(101%)	149 (96%)	6 (4%)	1 (1%)	25	27
2	С	149/154~(97%)	145 (97%)	4 (3%)	0	100	100
All	All	1298/1332~(97%)	1236 (95%)	56 (4%)	6 (0%)	34	32

All (6) Ramachandran outliers are listed below:

Mol	Chain	$\operatorname{Res}$	Type
1	А	545[A]	ASN
1	А	545[B]	ASN
1	А	746	SER
1	А	703	ASN
2	В	2	ALA
1	А	307	ASN

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	879/900~(98%)	839~(95%)	40 (5%)	27 32
2	В	140/136~(103%)	130 (93%)	10 (7%)	14 15
2	С	134/136~(98%)	124 (92%)	10 (8%)	13 13
All	All	1153/1172 (98%)	1093 (95%)	60 (5%)	23 27



All $(60)$ residues with a nor	-rotameric sidechain	are listed below:
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$\mathbf{Mol}$	Chain	$\operatorname{Res}$	Type
1	А	16	GLU
1	А	36	THR
1	А	79	GLN
1	А	96	ARG
1	А	120	LEU
1	А	130	ASP
1	А	147	SER
1	А	196	THR
1	А	202	ARG
1	А	263	LYS
1	А	294	LEU
1	А	309	GLU
1	А	339	GLU
1	А	349	LYS
1	А	410	THR
1	А	458	LEU
1	А	517	ILE
1	А	523	GLU
1	А	545[A]	ASN
1	А	545[B]	ASN
1	А	566	SER
1	А	589	SER
1	А	590	ARG
1	А	591	ASP
1	А	595	LYS
1	А	602	LEU
1	А	618	SER
1	А	657	SER
1	А	659	SER
1	А	716	THR
1	А	718	LEU
1	А	719	GLU
1	А	745	LYS
1	А	749	SER
1	А	756	ASP
1	А	796	ASP
1	А	815	LYS
1	А	880	GLU
1	А	930	ARG
1	А	932	ASP
2	В	1	MET
2	В	4	LEU



Mol	Chain	Res	Type
2	В	20	VAL
2	В	32	LEU
2	В	49	ASP
2	В	55	GLU
2	В	93	THR
2	В	125	VAL
2	В	145	LYS
2	В	151	LYS
2	С	10	LYS
2	С	18	ASP
2	С	33	ARG
2	С	70	ARG
2	С	71	PHE
2	С	82	ARG
2	С	89	ASP
2	С	119	ASP
2	С	125	VAL
2	С	145	LYS

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Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	541	ASN

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

8 ligands are modelled in this entry.



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In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mal	Turne	Fype Chain Bes Link		B	Bond lengths			Bond angles		
	Type	Unann	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	GOL	А	1104	-	$5,\!5,\!5$	0.86	0	$5,\!5,\!5$	0.96	0
3	SO4	А	1101	-	4,4,4	0.13	0	$6,\!6,\!6$	0.08	0
4	GOL	А	1106	-	$5,\!5,\!5$	0.76	0	$5,\!5,\!5$	1.08	0
3	SO4	А	1102	-	4,4,4	0.13	0	6,6,6	0.11	0
4	GOL	А	1103	-	$5,\!5,\!5$	0.80	0	$5,\!5,\!5$	0.87	0
4	GOL	А	1105	-	$5,\!5,\!5$	0.88	0	$5,\!5,\!5$	0.94	0
4	GOL	А	1108	-	$5,\!5,\!5$	0.84	0	$5,\!5,\!5$	0.90	0
4	GOL	А	1107	-	$5,\!5,\!5$	0.82	0	$5,\!5,\!5$	1.02	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	А	1104	-	-	2/4/4/4	-
4	GOL	А	1106	-	-	2/4/4/4	-
4	GOL	А	1103	-	-	2/4/4/4	-
4	GOL	А	1105	-	-	4/4/4/4	-
4	GOL	А	1108	-	-	4/4/4/4	-
4	GOL	А	1107	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	А	1104	GOL	C1-C2-C3-O3
4	А	1105	GOL	C1-C2-C3-O3
4	А	1107	GOL	C1-C2-C3-O3
4	А	1108	GOL	O1-C1-C2-O2



Mol	Chain	Res	Type	Atoms
4	А	1108	GOL	O1-C1-C2-C3
4	А	1103	GOL	O1-C1-C2-O2
4	А	1103	GOL	O1-C1-C2-C3
4	А	1106	GOL	O1-C1-C2-C3
4	А	1108	GOL	C1-C2-C3-O3
4	А	1105	GOL	O2-C2-C3-O3
4	А	1107	GOL	O2-C2-C3-O3
4	А	1104	GOL	O2-C2-C3-O3
4	А	1105	GOL	O1-C1-C2-O2
4	А	1105	GOL	O1-C1-C2-C3
4	А	1106	GOL	O1-C1-C2-O2
4	А	1108	GOL	O2-C2-C3-O3
4	А	1107	GOL	O1-C1-C2-O2

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There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	1103	GOL	2	0

## 5.7 Other polymers (i)

There are no such residues in this entry.

### 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



# 6 Fit of model and data (i)

## 6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median,  $95^{th}$  percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ $>$	#RSRZ>2	2	$\mathbf{OWAB}(\mathbf{A}^2)$	Q<0.9
1	А	994/1024~(97%)	0.53	86 (8%) 10	15	15,30,61,93	0
2	В	152/154~(98%)	0.54	10 (6%) 18	26	23, 38, 62, 82	0
2	С	151/154 (98%)	0.97	26 (17%) 1	2	26, 46, 74, 84	0
All	All	1297/1332~(97%)	0.58	122 (9%) 8	13	15, 33, 64, 93	0

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	749	SER	8.8
1	А	798	ILE	6.3
1	А	745	LYS	5.1
2	С	64	MET	4.9
1	А	812	ALA	4.9
1	А	813	GLY	4.4
2	С	2	ALA	4.4
2	С	89	ASP	4.3
1	А	746	SER	4.2
2	С	92	LYS	4.2
1	А	796	ASP	4.2
2	С	18	ASP	4.2
1	А	1011	GLU	4.1
2	В	150	LYS	4.0
2	С	93	THR	3.8
2	С	151	LYS	3.8
1	А	339	GLU	3.7
1	А	647	GLN	3.6
1	А	814	PHE	3.6
1	A	751	SER	3.6
2	В	149	LYS	3.6
2	С	29	ASP	3.5
1	А	773	ASN	3.5



Mol	Chain	Res	Type	RSRZ
1	А	646	LYS	3.5
2	С	134	GLN	3.4
1	А	771	THR	3.4
1	А	801	LEU	3.3
1	А	747	ASP	3.3
1	А	797	GLU	3.3
2	С	94	ASN	3.2
1	А	752	LYS	3.2
1	А	592	PRO	3.2
1	А	55	VAL	3.2
2	С	121	LEU	3.2
1	А	748	ASP	3.1
2	С	150	LYS	3.1
1	А	703	ASN	3.1
1	А	800	GLN	3.1
1	А	439	LEU	3.0
1	А	645	LEU	3.0
1	А	750	ASN	3.0
1	А	992	LYS	3.0
2	С	44	GLN	3.0
2	В	57	TYR	2.9
2	С	30	ASP	2.9
1	А	1010	LYS	2.9
2	В	18	ASP	2.9
1	А	594	GLU	2.9
2	С	120	PRO	2.9
2	С	3	SER	2.8
1	А	591	ASP	2.8
2	С	1	MET	2.8
2	В	2	ALA	2.8
1	А	245	GLU	2.7
1	А	881	LEU	2.7
1	А	799	ASP	2.7
1	А	10	ALA	2.7
1	А	795	SER	2.7
1	А	642	GLU	2.7
1	А	948	LYS	2.7
1	А	921	ASN	2.7
2	С	122	ALA	2.7
1	А	590	ARG	2.6
1	А	996	ALA	2.6
1	А	643	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	А	947	GLU	2.6
1	А	964	LEU	2.5
1	А	803	SER	2.5
1	А	540	THR	2.5
1	А	934	LYS	2.5
1	А	538	PHE	2.5
1	А	1003	LEU	2.5
1	А	510	LYS	2.5
2	В	17	SER	2.5
1	А	1005	ILE	2.5
1	А	56	VAL	2.5
1	А	544[A]	ASP	2.5
1	А	733	ALA	2.5
2	С	90	VAL	2.4
1	А	539	VAL	2.4
1	А	923	LYS	2.4
1	А	993	ASP	2.4
1	А	51	ILE	2.4
1	А	128	ALA	2.4
1	А	462	SER	2.4
1	А	595	LYS	2.3
1	А	802	VAL	2.3
1	А	11	ALA	2.3
1	А	115	ASP	2.3
1	А	920	ASN	2.3
1	А	308	GLY	2.2
1	А	39	VAL	2.2
1	А	453	TRP	2.2
1	А	995	PRO	2.2
1	A	221	LYS	2.2
1	A	374	VAL	2.2
1	A	296	PHE	2.2
1	А	650	ASP	2.2
2	С	87	CYS	2.2
1	А	244	LYS	2.2
2	В	34[A]	TYR	2.2
2	С	43	GLU	2.2
1	A	371	ALA	2.2
2	C	95	TRP	2.2
2	В	48	GLU	2.2
2	B	30	ASP	2.2
2	С	126	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	А	437	VAL	2.1
2	В	93	THR	2.1
1	А	48	GLY	2.1
1	А	840	CYS	2.1
1	А	675	TRP	2.1
1	А	730	PHE	2.1
2	С	130	ILE	2.1
1	А	735	ALA	2.1
1	А	57	LEU	2.0
2	С	141	ARG	2.0
2	С	149	LYS	2.0
1	А	438	PHE	2.0
1	А	1008	ASP	2.0
1	А	523	GLU	2.0
1	А	836	ALA	2.0

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### 6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

### 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
4	GOL	А	1103	6/6	0.83	0.21	34,42,51,53	0
4	GOL	А	1105	6/6	0.88	0.12	$27,\!33,\!37,\!38$	0
4	GOL	А	1107	6/6	0.88	0.17	27,34,46,46	0
4	GOL	А	1104	6/6	0.89	0.22	35,42,48,49	0
4	GOL	А	1108	6/6	0.89	0.35	36,44,49,49	0
4	GOL	А	1106	6/6	0.92	0.17	18,25,32,33	0
3	SO4	А	1102	5/5	0.95	0.14	31,31,35,39	0
3	SO4	А	1101	5/5	0.98	0.13	29,31,33,35	0



## 6.5 Other polymers (i)

There are no such residues in this entry.

